

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/808,124C  
Source: IFW16  
Date Processed by STIC: 5/11/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 05/11/2005

PATENT APPLICATION: US/09/808,124C

TIME: 08:53:33

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05112005\I808124C.raw

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5 <110> APPLICANT: Potter, Robert
6   Rosenthal, Kim
9 <120> TITLE OF INVENTION: High Fidelity Reverse Transcriptases and Uses Thereof
12 <130> FILE REFERENCE: 0942.5030001/RWE/HCC
15 <140> CURRENT APPLICATION NUMBER: 09/808,124C
17 <141> CURRENT FILING DATE: 2001-03-15
20 <150> PRIOR APPLICATION NUMBER: 60/189,454
22 <151> PRIOR FILING DATE: 2000-03-15
25 <160> NUMBER OF SEQ ID NOS: 6
28 <170> SOFTWARE: PatentIn version 3.0
32 <210> SEQ ID NO: 1
34 <211> LENGTH: 47
36 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
44 <223> OTHER INFORMATION: Synthetic oligonucleotide template
48 <400> SEQUENCE: 1
49 gagttacagt gtttttgttc cagtctgtag cagtgtgtga atggaag 47
52 <210> SEQ ID NO: 2
54 <211> LENGTH: 18
56 <212> TYPE: DNA
58 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
64 <223> OTHER INFORMATION: Synthetic oligonucleotide primer
68 <400> SEQUENCE: 2
69 cttccattca cacactgc 18
72 <210> SEQ ID NO: 3
74 <211> LENGTH: 21
76 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
84 <223> OTHER INFORMATION: Synthetic oligonucleotide primer
88 <400> SEQUENCE: 3
89 gaagatcgca ctccagccag c 21
92 <210> SEQ ID NO: 4
94 <211> LENGTH: 298
96 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
104 <223> OTHER INFORMATION: lacZa peptide in M13mp19 from SuperScript II RT and
105   SuperScript II H203R T306K F309N
109 <400> SEQUENCE: 4
110 agcgcaacgc aattaatgtg agttagctca ctcattaggc accccaggct ttacacttta 60

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112 tgcttcgaggc tcgtatgttg tgtggaattg tgagcggata acaatttcac acaggaaaca 120
114 gctatgacca tgattacgcc aagcttgcat gcctgcaggt cgactctaga ggatccccgg 180
116 gtaccgagct cgaattcact ggccgtcggt ttacaacgtc gtgactggga aaaccctggc 240
118 gttacccaac ttaatcgccct tgcagcacat ccccttttcg ccagctggcg taatagcg 298
122 <210> SEQ ID NO: 5
124 <211> LENGTH: 1515
126 <212> TYPE: DNA
128 <213> ORGANISM: Moloney-Murine Leukemia Virus
131 <220> FEATURE:
133 <221> NAME/KEY: CDS
135 <222> LOCATION: (1)..(1515)
137 <400> SEQUENCE: 5
139 atg acc cta aat ata gaa gat gag cat cgg cta cat gag acc tca aaa 48
140 Met Thr Leu Asn Ile Glu Asp Glu His Arg Leu His Glu Thr Ser Lys
141 1 5 10 15
143 gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag 96
144 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
145 20 25 30
147 gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct 144
148 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
149 35 40 45
151 ctg atc ata cct ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa 192
152 Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
153 50 55 60
155 tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag 240
156 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
157 65 70 75 80
159 aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac 288
160 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
161 85 90 95
163 acg ccc ctg cta ccc gtt aag aaa cca ggg act aat gat tat agg cct 336
164 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
165 100 105 110
167 gtc cag gat ctg aga gaa gtc aac aag cgg gtg gaa gac atc cac ccc 384
168 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
169 115 120 125
171 acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc cca ccg tcc cac 432
172 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
173 130 135 140
175 cag tgg tac act gtg ctt gat tta aag gat gcc ttt ttc tgc ctg aga 480
176 Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
177 145 150 155 160
179 ctc cac ccc acc agt cag cct ctc ttc gcc ttt gag tgg aga gat cca 528
180 Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
181 165 170 175
183 gag atg gga atc tca gga caa ttg acc tgg acc aga ctc cca cag ggt 576
184 Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
185 180 185 190
187 ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg cac aga gac cta 624

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188	Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu	His	Arg	Asp	Leu	
189			195					200					205				
191	gca	gac	ttc	cgg	atc	cag	cac	cca	gac	ttg	atc	ctg	cta	cag	tac	gtg	672
192	Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu	Leu	Gln	Tyr	Val	
193		210					215					220					
195	gat	gac	tta	ctg	ctg	gcc	gcc	act	tct	gag	cta	gac	tgc	caa	caa	ggg	720
196	Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp	Cys	Gln	Gln	Gly	
197	225					230					235					240	
199	act	cgg	gcc	ctg	tta	caa	acc	cta	ggg	aac	ctc	ggg	tat	cgg	gcc	tcg	768
200	Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asn	Leu	Gly	Tyr	Arg	Ala	Ser	
201						245				250					255		
203	gcc	aag	aaa	gcc	caa	att	tgc	cag	aaa	cag	gtc	aag	tat	ctg	ggg	tat	816
204	Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys	Tyr	Leu	Gly	Tyr	
205				260						265					270		
207	ctt	cta	aaa	gag	ggg	cag	aga	tgg	ctg	act	gag	gcc	aga	aaa	gag	act	864
208	Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala	Arg	Lys	Glu	Thr	
209			275					280					285				
211	gtg	atg	ggg	cag	cct	act	ccg	aag	acc	cct	cga	caa	cta	agg	gag	ttc	912
212	Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln	Leu	Arg	Glu	Phe	
213			290					295				300					
215	cta	ggg	acg	gca	ggc	ttc	tgt	cgc	ctc	tgg	atc	cct	ggg	ttt	gca	gaa	960
216	Leu	Gly	Thr	Ala	Gly	Phe	Cys	Arg	Leu	Trp	Ile	Pro	Gly	Phe	Ala	Glu	
217	305					310					315					320	
219	atg	gca	gcc	ccc	ttg	tac	cct	ctc	acc	aaa	acg	ggg	act	ctg	ttt	aat	1008
220	Met	Ala	Ala	Pro	Leu	Tyr	Pro	Leu	Thr	Lys	Thr	Gly	Thr	Leu	Phe	Asn	
221						325				330					335		
223	tgg	ggc	cca	gac	caa	caa	aag	gcc	tat	caa	gaa	atc	aag	caa	gct	ctt	1056
224	Trp	Gly	Pro	Asp	Gln	Gln	Lys	Ala	Tyr	Gln	Glu	Ile	Lys	Gln	Ala	Leu	
225				340					345				350				
227	cta	act	gcc	cca	gcc	ctg	ggg	ttg	cca	gat	ttg	act	aag	ccc	ttt	gaa	1104
228	Leu	Thr	Ala	Pro	Ala	Leu	Gly	Leu	Pro	Asp	Leu	Thr	Lys	Pro	Phe	Glu	
229			355					360					365				
231	ctc	ttt	gtc	gac	gag	aag	cag	ggc	tac	gcc	aaa	ggg	gtc	cta	acg	caa	1152
232	Leu	Phe	Val	Asp	Glu	Lys	Gln	Gly	Tyr	Ala	Lys	Gly	Val	Leu	Thr	Gln	
233		370					375					380					
235	aaa	ctg	gga	cct	tgg	cgt	cgg	ccg	gtg	gcc	tac	ctg	tcc	aaa	aag	cta	1200
236	Lys	Leu	Gly	Pro	Trp	Arg	Arg	Pro	Val	Ala	Tyr	Leu	Ser	Lys	Lys	Leu	
237	385					390					395					400	
239	gac	cca	gta	gca	gct	ggg	tgg	ccc	cct	tgc	cta	cgg	atg	gta	gca	gcc	1248
240	Asp	Pro	Val	Ala	Ala	Gly	Trp	Pro	Pro	Cys	Leu	Arg	Met	Val	Ala	Ala	
241						405				410					415		
243	att	gcc	gta	ctg	aca	aag	gat	gca	ggc	aag	cta	acc	atg	gga	cag	cca	1296
244	Ile	Ala	Val	Leu	Thr	Lys	Asp	Ala	Gly	Lys	Leu	Thr	Met	Gly	Gln	Pro	
245				420					425					430			
247	cta	gtc	att	ctg	gcc	ccc	cat	gca	gta	gag	gca	cta	gtc	aaa	caa	ccc	1344
248	Leu	Val	Ile	Leu	Ala	Pro	His	Ala	Val	Glu	Ala	Leu	Val	Lys	Gln	Pro	
249			435					440					445				
251	ccc	gac	cgc	tgg	ctt	tcc	aac	gcc	cgg	atg	act	cac	tat	cag	gcc	ttg	1392
252	Pro	Asp	Arg	Trp	Leu	Ser	Asn	Ala	Arg	Met	Thr	His	Tyr	Gln	Ala	Leu	

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253      450      455      460
255 ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg gta gcc ctg aac      1440
256 Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
257 465      470      475      480
259 ccg gct acg ctg ctc cca ctg cct gag gaa ggg ctg caa cac aac tgc      1488
260 Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
261      485      490      495
263 ctt gat aat tcc cgc tta att aat taa      1515
264 Leu Asp Asn Ser Arg Leu Ile Asn
265      500
268 <210> SEQ ID NO: 6
270 <211> LENGTH: 504
272 <212> TYPE: PRT
274 <213> ORGANISM: Moloney Murine Leukemia Virus
277 <400> SEQUENCE: 6
279 Met Thr Leu Asn Ile Glu Asp Glu His Arg Leu His Glu Thr Ser Lys
280 1      5      10      15
283 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
284      20      25      30
287 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
288      35      40      45
291 Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
292      50      55      60
295 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
296 65      70      75      80
299 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
300      85      90      95
303 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
304      100      105      110
307 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
308      115      120      125
311 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
312      130      135      140
315 Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
316 145      150      155      160
319 Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
320      165      170      175
323 Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
324      180      185      190
327 Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu His Arg Asp Leu
328      195      200      205
331 Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
332      210      215      220
335 Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
336 225      230      235      240
339 Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly Tyr Arg Ala Ser
340      245      250      255
343 Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
344      260      265      270

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347 Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
348           275           280           285
351 Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
352           290           295           300
355 Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu
356 305           310           315           320
359 Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
360           325           330           335
363 Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
364           340           345           350
367 Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu
368           355           360           365
371 Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
372           370           375           380
375 Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
376 385           390           395           400
379 Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
380           405           410           415
383 Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
384           420           425           430
387 Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
388           435           440           445
391 Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
392           450           455           460
395 Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
396 465           470           475           480
399 Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
400           485           490           495
403 Leu Asp Asn Ser Arg Leu Ile Asn
404           500

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**VERIFICATION SUMMARY**

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